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1642

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/763,985A

DATE: 11/25/2001
TIME: 14:05:11

Input Set : A:\0020-4817P.ST25.txt
Output Set: N:\CRF3\11212001\I763985A.raw

3 <110> APPLICANT: ITOH, Kyogo et al.
5 <120> TITLE OF INVENTION: NOVEL TUMOR ANTIGEN PROTEIN SART-13 AND TUMOR ANTIGEN PEPTIDES THEREOF

ENTERED

7 <130> FILE REFERENCE: 0020-4817P
9 <140> CURRENT APPLICATION NUMBER: 09/763,985A
10 <141> CURRENT FILING DATE: 2001-02-28
12 <160> NUMBER OF SEQ ID NOS: 64
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 3798
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (12)..(2900)
24 <223> OTHER INFORMATION:
27 <400> SEQUENCE: 1

TECH CENTER 1600/2900

DEC 18 2001

RECEIVED

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29			Met	Ala	Thr	Ala	Ala	Glu	Thr	Ser	Ala	Ser	Glu	Pro	Glu		
30			1				5				10						
32	gct	gag	tcc	aag	gct	ggg	ccc	aag	gct	gac	gga	gag	gag	gat	gag	98	
33	Ala	Glu	Ser	Lys	Ala	Gly	Pro	Lys	Ala	Asp	Gly	Glu	Glu	Asp	Glu	Val	
34	15					20					25						
36	aag	gcg	gct	agg	aca	agg	aga	aag	gtg	tta	tcg	cgg	gct	gtg	gcc	gct	146
37	Lys	Ala	Ala	Arg	Thr	Arg	Arg	Lys	Val	Leu	Ser	Arg	Ala	Val	Ala	Ala	
38	30					35				40		45					
40	gcg	aca	tac	aag	acc	atg	ggg	cca	gcg	tgg	gat	cag	cag	gag	gaa	ggc	194
41	Ala	Thr	Tyr	Lys	Thr	Met	Gly	Pro	Ala	Trp	Asp	Gln	Gln	Glu	Glu	Gly	
42						50			55		60						
44	gtg	agc	gag	agc	gat	ggg	gat	gag	tac	gcc	atg	gct	tcc	tcc	gcg	gag	242
45	Val	Ser	Glu	Ser	Asp	Gly	Asp	Glu	Tyr	Ala	Met	Ala	Ser	Ser	Ala	Glu	
46	65					70				75							
48	agc	tcc	ccc	ggg	gag	tac	gag	tgg	gaa	tat	gac	gaa	gag	gag	aaa	290	
49	Ser	Ser	Pro	Gly	Glu	Tyr	Glu	Trp	Glu	Tyr	Asp	Glu	Glu	Glu	Glu	Lys	
50	80					85			90								
52	aac	cag	ctg	gag	att	gag	aga	ctg	gag	gag	cag	ttg	tct	atc	aac	gtc	338
53	Asn	Gln	Leu	Glu	Ile	Glu	Arg	Leu	Glu	Glu	Gln	Leu	Ser	Ile	Asn	Val	
54	95					100			105								
56	tat	gac	tac	aac	tgc	cat	gtg	gac	ttg	atc	aga	ctg	ctc	agg	ctg	gaa	386
57	Tyr	Asp	Tyr	Asn	Cys	His	Val	Asp	Leu	Ile	Arg	Leu	Leu	Arg	Leu	Glu	
58	110					115			120			125					
60	ggg	gag	ctt	acc	aag	gtg	agg	atg	gcc	cgc	cag	aag	atg	agt	gaa	atc	434
61	Gly	Glu	Leu	Thr	Lys	Val	Arg	Met	Ala	Arg	Gln	Lys	Met	Ser	Glu	Ile	
62						130			135			140					
64	ttt	ccc	ttg	act	gaa	gag	ctc	tgg	ctg	gag	tgg	ctg	cat	gac	gag	atc	482
65	Phe	Pro	Leu	Thr	Glu	Glu	Leu	Trp	Leu	Glu	Trp	Leu	His	Asp	Glu	Ile	
66	145					150			155								
68	agc	atg	gcc	cag	gat	ggc	ctg	gac	aga	gag	cac	gtg	tat	gac	ctc	ttt	530

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70		160			165					170							
72	gag	aaa	gcc	gtg	aag	gat	tac	att	tgt	cct	aac	att	tgg	cta	gag	tat	578
73	Glu	Lys	Ala	Val	Lys	Asp	Tyr	Ile	Cys	Pro	Asn	Ile	Trp	Leu	Glu	Tyr	
74		175			180					185							
76	ggc	cag	tac	tca	gtt	ggg	att	ggt	cag	aaa	ggt	ggc	ctt	gag	aaa		626
77	Gly	Gln	Tyr	Ser	Val	Gly	Gly	Ile	Gly	Gln	Lys	Gly	Gly	Leu	Glu	Lys	
78	190		195			200					205						
80	gtt	cgc	tcc	gtg	ttt	gaa	agg	gct	ctc	tcg	tct	gtt	ggt	tta	cat	atg	674
81	Val	Arg	Ser	Val	Phe	Glu	Arg	Ala	Leu	Ser	Ser	Val	Gly	Leu	His	Met	
82		210			215					220							
84	acc	aaa	gga	ctc	gcc	ctc	tgg	gag	gct	tac	cga	gag	ttt	gaa	agt	gcg	722
85	Thr	Lys	Gly	Leu	Ala	Leu	Trp	Glu	Ala	Tyr	Arg	Glu	Phe	Glu	Ser	Ala	
86		225			230					235							
88	att	gtg	gaa	gct	gtc	ggg	ctt	gag	aaa	gtc	cac	agt	ttt	ttc	cgg	cga	770
89	Ile	Val	Glu	Ala	Ala	Arg	Leu	Glu	Lys	Val	His	Ser	Leu	Phe	Arg	Arg	
90		240			245					250							
92	cag	ttg	gcg	atc	cca	ctc	tat	gat	atg	gag	gcc	aca	ttt	gca	gag	tat	818
93	Gln	Leu	Ala	Ile	Pro	Leu	Tyr	Asp	Met	Glu	Ala	Thr	Phe	Ala	Glu	Tyr	
94		255			260					265							
96	gaa	gaa	tgg	tca	gaa	gac	cca	ata	cca	gag	tca	gta	att	cag	aac	tat	866
97	Glu	Glu	Trp	Ser	Glu	Asp	Pro	Ile	Pro	Glu	Ser	Val	Ile	Gln	Asn	Tyr	
98	270		275			280					285						
100	aac	aaa	gca	cta	cag	cag	ctg	gag	aaa	tat	aaa	ccc	tat	gaa	gaa	gca	914
101	Asn	Lys	Ala	Leu	Gln	Gln	Leu	Glu	Lys	Tyr	Lys	Pro	Tyr	Glu	Glu	Ala	
102		290			295					300							
104	ctg	ttg	cag	gca	gag	gca	cca	agg	ctg	gca	gaa	tat	caa	gca	tat	atc	962
105	Leu	Leu	Gln	Ala	Glu	Ala	Pro	Arg	Leu	Ala	Glu	Tyr	Gln	Ala	Tyr	Ile	
106		305			310					315							
108	gat	ttt	gag	atg	aaa	att	ggc	gat	cct	gct	cgc	att	cag	ttg	atc	ttt	1010
109	Asp	Phe	Glu	Met	Lys	Ile	Gly	Asp	Pro	Ala	Arg	Ile	Gln	Leu	Ile	Phe	
110		320			325					330							
112	gag	cgc	gcc	ctg	gtc	gag	aac	tgc	ctt	gtc	cca	gac	tta	tgg	atc	cgt	1058
113	Glu	Arg	Ala	Leu	Val	Glu	Asn	Cys	Leu	Val	Pro	Asp	Leu	Trp	Ile	Arg	
114		335			340					345							
116	tac	agt	cag	tac	cta	gat	cga	caa	ctg	aaa	gta	aag	gat	ttg	gtt	tta	1106
117	Tyr	Ser	Gln	Tyr	Leu	Asp	Arg	Gln	Leu	Lys	Val	Lys	Asp	Leu	Val	Leu	
118	350		355			360					365						
120	tct	gta	cat	aac	cgc	gct	att	aga	aac	tgc	ccc	tgg	aca	gtt	gcc	tta	1154
121	Ser	Val	His	Asn	Arg	Ala	Ile	Arg	Asn	Cys	Pro	Trp	Thr	Val	Ala	Leu	
122		370			375					380							
124	tgg	agt	cgg	tac	ctc	ttg	gcc	atg	gag	aga	cat	gga	gtt	gat	cat	caa	1202
125	Trp	Ser	Arg	Tyr	Leu	Leu	Ala	Met	Glu	Arg	His	Gly	Val	Asp	His	Gln	
126		385			390					395							
128	gta	att	tct	gta	acc	ttc	gag	aaa	gct	ttg	aat	gcc	ggc	ttc	atc	cag	1250
129	Val	Ile	Ser	Val	Thr	Phe	Glu	Lys	Ala	Leu	Asn	Ala	Gly	Phe	Ile	Gln	
130		400			405					410							
132	gcc	act	gat	tat	gtg	gag	att	tgg	cag	gca	tac	ctt	gat	tac	ctg	agg	1298
133	Ala	Thr	Asp	Tyr	Val	Glu	Ile	Trp	Gln	Ala	Tyr	Leu	Asp	Tyr	Leu	Arg	

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134	415	420	425	
136	aga agg gtt gat ttc aaa caa gac tcc agt aaa gag ctg gag gag ttg			1346
137	Arg Arg Val Asp Phe Lys Gln Asp Ser Ser Lys Glu Leu Glu Glu Leu			
138	430	435	440	445
140	agg gcc gcc ttt act cgt gcc ttg gag tat ctg aag cag gag gtg gaa			1394
141	Arg Ala Ala Phe Thr Arg Ala Leu Glu Tyr Leu Lys Gln Glu Val Glu			
142	450	455	460	
144	gag cgt ttc aat gag agt ggt gat cca agc tgc gtg att atg cag aac			1442
145	Glu Arg Phe Asn Glu Ser Gly Asp Pro Ser Cys Val Ile Met Gln Asn			
146	465	470	475	
148	tgg gct agg att gag gct cga ctg tgc aat aac atg cag aaa gct cgg			1490
149	Trp Ala Arg Ile Glu Ala Arg Leu Cys Asn Asn Met Gln Lys Ala Arg			
150	480	485	490	
152	gaa ctc tgg gat agc atc atg acc aga gga aat gcc aag tac gcc aac			1538
153	Glu Leu Trp Asp Ser Ile Met Thr Arg Gly Asn Ala Lys Tyr Ala Asn			
154	495	500	505	
156	atg tgg cta gag tat tac aac ctg gaa aga gct cat ggt gac acc cag			1586
157	Met Trp Leu Glu Tyr Tyr Asn Leu Glu Arg Ala His Gly Asp Thr Gln			
158	510	515	520	525
160	cac tgc cgg aag gct ctg cac cgg gcc gtc cag tgc acc agt gac tac			1634
161	His Cys Arg Lys Ala Leu His Arg Ala Val Gln Cys Thr Ser Asp Tyr			
162	530	535	540	
164	cca gag cac gtc tgc gaa gtg tta ctc acc atg gag agg aca gaa ggt			1682
165	Pro Glu His Val Cys Glu Val Leu Leu Thr Met Glu Arg Thr Glu Gly			
166	545	550	555	
168	tct tta gaa gat tgg gat ata gct gtt cag aaa act gaa acc cga tta			1730
169	Ser Leu Glu Asp Trp Asp Ile Ala Val Gln Lys Thr Glu Thr Arg Leu			
170	560	565	570	
172	gct cgt gtc aat gag cag aga atg aag gct gca gag aag gaa gca gcc			1778
173	Ala Arg Val Asn Glu Gln Arg Met Lys Ala Ala Glu Lys Glu Ala Ala			
174	575	580	585	
176	ctt gtg cag caa gaa gaa aag gct gaa caa cgg aaa aga gct cgg			1826
177	Leu Val Gln Gln Glu Glu Lys Ala Glu Gln Arg Lys Arg Ala Arg			
178	590	595	600	605
180	gct gag aag aaa gcg tta aaa aag aag aaa aag atc aga ggc cca gag			1874
181	Ala Glu Lys Lys Ala Leu Lys Lys Lys Lys Ile Arg Gly Pro Glu			
182	610	615	620	
184	aag cgc gga gca gat gag gac gat gag aaa gag tgg ggc gat gat gaa			1922
185	Lys Arg Gly Ala Asp Glu Asp Asp Glu Lys Glu Trp Gly Asp Asp Glu			
186	625	630	635	
188	gaa gag cag cct tcc aaa cgc aga agg gtc gag aac agc atc cct gca			1970
189	Glu Glu Gln Pro Ser Lys Arg Arg Arg Val Glu Asn Ser Ile Pro Ala			
190	640	645	650	
192	gct gga gaa aca caa aat gta gaa gta gca gca ggg ccc gct ggg aaa			2018
193	Ala Gly Glu Thr Gln Asn Val Glu Val Ala Ala Gly Pro Ala Gly Lys			
194	655	660	665	
196	tgt gct gcc gta gat gtg gag ccc cct tcg aag cag aag gag aag gca			2066
197	Cys Ala Ala Val Asp Val Glu Pro Pro Ser Lys Gln Lys Glu Lys Ala			
198	670	675	680	685

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201	Ala Ser Leu Lys Arg Asp Met Pro Lys Val Leu His Asp Ser Ser Lys	
202	690 695 700	
204	gac agc atc acc gtc ttt gtc agc aac ctg ccc tac agc atg cag gag	2162
205	Asp Ser Ile Thr Val Phe Val Ser Asn Leu Pro Tyr Ser Met Gln Glu	
206	705 710 715	
208	ccg gac acg aag ctc agg cca ctc ttc gag gcc tgt ggg gag gtg gtc	2210
209	Pro Asp Thr Lys Leu Arg Pro Leu Phe Glu Ala Cys Gly Glu Val Val	
210	720 725 730	
212	cag atc cga ccc atc ttc agc aac cgt ggg gat ttc cga ggt tac tgc	2258
213	Gln Ile Arg Pro Ile Phe Ser Asn Arg Gly Asp Phe Arg Gly Tyr Cys	
214	735 740 745	
216	tac gtg gag ttt aaa gaa gag aaa tca gcc ctt cag gca ctg gag atg	2306
217	Tyr Val Glu Phe Lys Glu Glu Lys Ser Ala Leu Gln Ala Leu Glu Met	
218	750 755 760 765	
220	gac cg ^g aaa agt gta gaa ggg agg cca atg ttt gtt tcc ccc tgt gtg	2354
221	Asp Arg Lys Ser Val Glu Gly Arg Pro Met Phe Val Ser Pro Cys Val	
222	770 775 780	
224	gat aag agc aaa aac ccc gat ttt aag gtg ttc agg tac agc act tcc	2402
225	Asp Lys Ser Lys Asn Pro Asp Phe Lys Val Phe Arg Tyr Ser Thr Ser	
226	785 790 795	
228	cta gag aaa cac aag ctg ttc atc tca ggc ctg cct ttc tcc tgt act	2450
229	Leu Glu Lys His Lys Leu Phe Ile Ser Gly Leu Pro Phe Ser Cys Thr	
230	800 805 810	
232	aaa gag gaa cta gaa gaa atc tgt aag gct cat ggc acc gtg aag gac	2498
233	Lys Glu Glu Leu Glu Ile Cys Lys Ala His Gly Thr Val Lys Asp	
234	815 820 825	
236	ctc agg ctg gtc acc aac cgg gct ggc aaa cca aag ggc ctg gcc tac	2546
237	Leu Arg Leu Val Thr Asn Arg Ala Gly Lys Pro Lys Gly Leu Ala Tyr	
238	830 835 840 845	
240	gtg gag tat gaa aat gaa tcc cag gc ^g tc ^g cag gct gtg atg aag atg	2594
241	Val Glu Tyr Glu Asn Glu Ser Gln Ala Ser Gln Ala Val Met Lys Met	
242	850 855 860	
244	gac ggc atg act atc aaa gag aac atc atc aaa gtg gca atc agc aac	2642
245	Asp Gly Met Thr Ile Lys Glu Asn Ile Ile Lys Val Ala Ile Ser Asn	
246	865 870 875	
248	cct cct cag agg aaa gtt cca gag aag cca gag acc agg aag gca cca	2690
249	Pro Pro Gln Arg Lys Val Pro Glu Lys Pro Glu Thr Arg Lys Ala Pro	
250	880 885 890	
252	ggt ggc ccc atg ctt ttg ccg cag aca tac gga gc ^g agg ggg aag gga	2738
253	Gly Gly Pro Met Leu Leu Pro Gln Thr Tyr Gly Ala Arg Gly Lys Gly	
254	895 900 905	
256	agg acg cag ctg tct cta ctg cct cgt gcc ctg cag cgc cca agt gct	2786
257	Arg Thr Gln Leu Ser Leu Leu Pro Arg Ala Leu Gln Arg Pro Ser Ala	
258	910 915 920 925	
260	gca gct cct cag gct gag aac ggc cct gcc gc ^g gct cct gca gtt gcc	2834
261	Ala Ala Pro Gln Ala Glu Asn Gly Pro Ala Ala Ala Pro Ala Val Ala	
262	930 935 940	
264	gcc cca gca gcc acc gag gca ccc aag atg tcc aat gcc gat ttt gcc	2882

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268	aag	ctg	ttt	ctg	aga	aag	tgaacgggac	gctgggagac	aggaaatgcc							2930	
269	Lys	Leu	Phe	Leu	Arg	Lys											
270										960							
272	ttacttcact	ctggcccggc	ggacctccca	ccacccagca	gtgcactggg	gatggacagg										2990	
274	cctggtgtgc	tgcgtgc	caaccacaga	tggctcctcg	gcttttagaca	gaaaggggaa										3050	
276	ggggttctaa	gtcaagagcc	tttcagtgt	ccctcatatt	gagggcagtg	gcagaaaaagt										3110	
278	gaccactctg	caggctgggc	ccaggatgtg	gtgtcctgag	atagtttgtt	atcttaaga										3170	
280	ctgaggcaca	gaagcggaaac	gagaacacac	tgtttttgag	acacagtgt	ccaaatgttt										3230	
282	ctggccagct	ccggccccctt	tttgtatgac	acttctcttc	caccotgcac	agcacatgtg										3290	
284	cccgtcattc	ttttaatttt	aaaagatgaa	atggcagatg	ctagtaattc	acagaatggc										3350	
286	ctcttgggg	ggtgggtctg	agggaaagtca	gctataaaac	atttgctgga	gttttggcca										3410	
288	atggggctgt	gcatttttat	attatgtgtt	tgtaaatgac	atgtcagccc	ttgtttcatg										3470	
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294	gccctttgg	tttggtaat	accatgtcaa	atgcaaactt	caattctccc	catttagctt										3650	
296	tattaaactg	acgttctctt	caaaacttct	tgctgaatgg	tactcagatg	tgcattcaca										3710	
298	tacagatgt	ttttgaagtg	ggtgtacctt	gcttaccta	atagatgtgt	aaatagaact										3770	
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315						20				25						30	
318	Arg	Thr	Arg	Arg	Lys	Val	Leu	Ser	Arg	Ala	Val	Ala	Ala	Ala	Ala	Thr	Tyr
319						35				40						45	
322	Lys	Thr	Met	Gly	Pro	Ala	Trp	Asp	Gln	Gln	Glu	Glu	Gly	Val	Ser	Glu	
323						50				55						60	
326	Ser	Asp	Gly	Asp	Glu	Tyr	Ala	Met	Ala	Ser	Ser	Ala	Glu	Ser	Ser	Pro	
327						65				70						80	
330	Gly	Glu	Tyr	Glu	Trp	Glu	Tyr	Asp	Glu	Glu	Glu	Glu	Lys	Asn	Gln	Leu	
331						85				90						95	
334	Glu	Ile	Glu	Arg	Leu	Glu	Glu	Gln	Leu	Ser	Ile	Asn	Val	Tyr	Asp	Tyr	
335						100				105						110	
338	Asn	Cys	His	Val	Asp	Leu	Ile	Arg	Leu	Leu	Arg	Leu	Glu	Gly	Glu	Leu	
339						115				120						125	
342	Thr	Lys	Val	Arg	Met	Ala	Arg	Gln	Lys	Met	Ser	Glu	Ile	Phe	Pro	Leu	
343						130				135						140	
346	Thr	Glu	Glu	Leu	Trp	Leu	Glu	Trp	Leu	His	Asp	Glu	Ile	Ser	Met	Ala	
347						145				150						160	
350	Gln	Asp	Gly	Leu	Asp	Arg	Glu	His	Val	Tyr	Asp	Leu	Phe	Glu	Lys	Ala	
351						165				170						175	
354	Val	Lys	Asp	Tyr	Ile	Cys	Pro	Asn	Ile	Trp	Leu	Glu	Tyr	Gly	Gln	Tyr	
355						180				185						190	

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/763,985A

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Output Set: N:\CRF3\11212001\I763985A.raw

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L:1256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
L:1282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:1308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
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L:1386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64